#5

Attorney's Docket No.: 12125-002001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Jan Johansson
Serial No. : 09/988,842
Filed : November 19, 2001
Title : DISCORDANT HELIX STABILIZATION FOR PREVENTION OF AMYLOID FORMATION

Art Unit : 1711
Examiner : Unknown

BOX MISSING PARTS
U.S. Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

PRELIMINARY AMENDMENT

In response to the communication dated February 13, 2002 (copy enclosed), applicant submits herewith a Sequence Listing in computer readable form as required by 37 CFR §1.824. In addition, applicant submits an initial Sequence Listing as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f).

Applicant respectfully requests entry of the paper copy and computer readable copy of the Sequence Listing filed herewith for the instant application. Furthermore, applicant requests entry of the following amendments.

In the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the U.S. Patent and Trademark Office, P.O. Box 2327, Arlington, VA 22202.

4/12/02
Date of Deposit

Signature

K Hutchins
Typed or Printed Name of Person Signing Certificate

Replace the paragraph beginning at page 6, line 4, with the following rewritten paragraph:

--Figs. 2A-2B are a set of diagrams that depict the characteristics of long discordant helix segments. Amino acid sequences, together with determined and predicted secondary structure elements for sequences having ≥9=residue discordant segments are shown. Also shown are those discordant segments of Aβ, mouse PrP, and human PrP. The proteins are grouped by the length of their discordant stretch. The experimentally determined helical segments are drawn as blue cylinders in the bottom row of each case in which the amino acid sequences and residue positions in the PDB entries of the corresponding proteins are given (Top to bottom in each set: Set 16 contains SEQ ID NOs:4-6; Set 15 contains SEQ ID NOs:7 and 8; Set 8 contains SEQ ID NO:9; Set 13 contains SEQ ID NOs:10 and 11; Set 12 contains SEQ ID NOs:12 and 13; Set 10 contains SEQ ID NOs:14 and 15; Set 11 contains SEQ ID NOs:16-18; Set 9 contains SEQ ID NOs:19-20 (top row left to right) and 21-23 (bottom row left to right). The locations of the β-strands predicted by PHD are visualized by yellow strands in the middle row of each case, wherein the reliability index for each residue is shown. The Chou-Fasman-based predictions averaged for 6-residue segments are plotted above residue 3 in each segment and given in the top row of each case. E and e denote extended structures (i.e., β-strands) predicted with high and low probability, respectively, as in Chou and Fasman (1978, Adv. Enzymol. 47:45-148), and H and h represent predicted helical structures in an analogous manner.--

Replace the paragraph beginning at page 6, line 18, with the following rewritten paragraph:

--Fig. 3 is a diagram that depicts the amino acid sequence (bottom row; SEQ ID NO:24) and predicted secondary structure by PHD and according to Chou-Fasman analysis for a polyleucine analogue of SP-C (lung surfactant protein C). The PHD predictions including reliability indices are given in the middle row and the Chou-Fasman data in the top row, but in this case an α-helix is predicted by both methods, symbolized by a blue cylinder for the PHD prediction.--

Replace the paragraph beginning at page 6, line 27, with the following rewritten paragraph:

--Fig. 5 is a set of diagrams that depict the experimentally determined and predicted secondary structures of positions 1-28 of Aβ (SEQ ID NO:25; top) and a variant of Aβ (1-28) in which three residues have been changed to alanine (K16A, L17A, F20A) (SEQ ID NO:26; bottom). Symbols are as described for Figs. 2 and 4.--

<u>In the drawings</u>:

Substitute the enclosed fourteen sheets of formal drawings for the original informal drawings filed with the application.

REMARKS

Applicant hereby submits that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely insert the paper copy of the Sequence Listing and sequence identifiers in the specification, and replace the informal drawings with formal drawings. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket number 12125-002001.

Respectfully submitted,

Date: 12 April 2002

Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819
Anita Meiklejohn
Reg. No. 35,283

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20419431.doc

"Version With Markings to Show Changes Made"

In the specification:

Paragraph beginning at page 6, line 4, has been amended as follows:

[Fig. 2 is] Figs. 2A-2B are a set of diagrams that depict the characteristics of long discordant helix segments. Amino acid sequences, together with determined and predicted secondary structure elements for sequences having ≥9=residue discordant segments are shown. Also shown are those discordant segments of Aβ, mouse PrP, and human PrP. The proteins are grouped by the length of their discordant stretch. The experimentally determined helical segments are drawn as blue cylinders in the bottom row of each case in which the amino acid sequences and residue positions in the PDB entries of the corresponding proteins are given (Top to bottom in each set: Set 16 contains SEQ ID NOs:4-6; Set 15 contains SEQ ID NOs:7 and 8; Set 8 contains SEQ ID NO:9; Set 13 contains SEQ ID NOs:10 and 11; Set 12 contains SEQ ID NOs:12 and 13; Set 10 contains SEQ ID NOs:14 and 15; Set 11 contains SEQ ID NOs:16-18; Set 9 contains SEQ ID NOs:19-20 (top row left to right) and 21-23 (bottom row left to right). The locations of the β-strands predicted by PHD are visualized by yellow strands in the middle row of each case, wherein the reliability index for each residue is shown. The Chou-Fasman-based predictions averaged for 6-residue segments are plotted above residue 3 in each segment and given in the top row of each case. E and e denote extended structures (i.e., β-strands) predicted with high and low probability, respectively, as in Chou and Fasman (1978, Adv. Enzymol. 47:45-148), and H and h represent predicted helical structures in an analogous manner.

Paragraph beginning at page 6, line 18, has been amended as follows:

Fig. 3 is a diagram that depicts the amino acid sequence (bottom row; SEQ ID NO:24) and predicted secondary structure by PHD and according to Chou-Fasman analysis for a polyleucine analogue of SP-C (lung surfactant protein C). The PHD predictions including reliability indices are given in the middle row and the Chou-Fasman data in the top row, but in this case an α-helix is predicted by both methods, symbolized by a blue cylinder for the PHD prediction.

Paragraph beginning at page 6, line 27, has been amended as follows:

Fig. 5 is a set of diagrams that depict the experimentally determined and predicted secondary structures of positions 1-28 of Aβ <u>(SEQ ID NO:25; top)</u> and a variant of Aβ (1-28) in which three residues have been changed to alanine (K16A, L17A, F20A) <u>(SEQ ID NO:26; bottom)</u>. Symbols are as described for Figs. 2 and 4.